

A;Cross-references: EMBL:U08024; NID:9468250; PIDN:AA17749.1; PID:9468251
 A;Accession: 138549
 A;Status: translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-285 <OTI2>
 A;Note: parts of this sequence were determined by protein sequencing; the amino end of t
 A;Note: three electrophoretic forms were observed
 R;Kong, A.N.T.; Yang, L.; Ma, M.; Tao, D.; Björnsson, T.D.
 Biochem. Biophys. Res. Commun. 187, 448-454, 1992.
 A;Title: Molecular cloning of the alcohol/hydroxysteroid form (hsra) of sulfotransferase
 A;Reference number: JCL223; MUID:9239364; PMID:1520333
 A;Accession: JCL223
 A;Molecule type: mRNA
 A;Residues: 1-158; V, 160-285 <KON>
 A;Cross-references: GB:SA43859; NID:9255072
 A;Experimental source: liver
 A;Note: the authors translated the codon AGC for residue 222 as Thr
 R;Comer, K.A.; Falany, J.L.; Falany, C.N.
 Biochem. J. 289, 233-240, 1993
 A;Title: Cloning and expression of human liver dehydroepiandrosterone sulphotransferase
 A;Reference number: S28155; MUID:93143674; PMID:7678732
 A;Accession: S28155
 A;Molecule type: mRNA
 A;Residues: 1-89, 'S', 91-285 <COM>
 A;Cross-references: GB:X0222; GB:S53620; NID:9312804; PIDN:CAA49755.1; PID:9312805; GB:
 A;Note: parts of this sequence were determined by protein sequencing; the amino end of t
 R;Forbes, K.J.; Hagen, M.; Glatt, H.; Hume, R.; Coughtrie, M.W.
 MOL Cell. Endocrinol. 112, 53-60, 1995
 A;Title: Human fetal adrenal hydroxysteroid sulphotransferase: cDNA cloning, stable expr
 A;Reference number: A58735
 A;Accession: A58735
 A;Molecule type: mRNA
 A;Residues: 1-285 <FOR>
 A;Cross-references: GB:X84816; NID:9683577; PIDN:CAA59274.1; PID:9683578
 A;Experimental source: fetal adrenal
 R;Ottermann, D.M.; Her, C.; Aksoy, S.; Kimura, S.; Wieben, E.D.; Weinshilboum, R.M.
 DNA Cell Biol. 14, 331-341, 1995
 A;Title: Human dehydroepiandrosterone sulfotransferase gene: molecular cloning and struc
 A;Reference number: I37285; MUID:95225980; PMID:7710689
 A;Accession: I37285
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-285 <RES>
 A;Cross-references: EMBL:U13061; NID:9806716; PIDN:AA51353.1; PID:9806718
 C;Genetics:
 A;Gene: GDB:STD; HST
 A;Cross-references: GDB:132655; OMIM:125263
 A;Map position: 19q13.3-19q13.3
 A;Introns: 46/1; 115/3; 158/1; 189/3; 249/1.
 C;Complex: homodimer
 C;Function:
 A;Description: catalyzes formation of the sulfate esters of alcohols using 3'-phosphoade
 A;Pathway: steroid metabolism; detoxification
 A;Note: sulfatases bile acids and steroids, in particular dehydroepiandrosterone, in the 1
 C;Superfamily: alcohol sulfotransferase
 C;Keywords: acetylated amino end; detoxification; homodimer; steroid metabolism; sulfot
 F;2;Modified site: acetylated amino end (Ser) (in mature form) #status predicted
 Query Match 9.9%; Score 8; DB 1; Length 285;
 Best Local Similarity 10.0%; Pred. No. 1.2; Length 285;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 48 FRSETLRK 55
 Db 18 FRSETLRK 25
 RESULT 3
 A;Accession: 144201
 A;Title: artifact-warning sequence (translated ALU class A) - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
 R;Claverie, J.M.
 Personal communication, 1992
 A;Reference number: A40201
 A;Accession: A40201
 A;Molecule type: DNA
 A;Residues: 1-627 <CLIA>
 R;Claverie, J.M.
 Genomics 12, 838-841, 1992
 A;Title: Identifying coding exons by similarity search: Alu-derived and other potent
 A;Reference number: A40200; MUID:92241891; PMID:1572661
 A;Contents: annotation
 C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames o
 In frame stop codons are shown as 'X'.
 C;Comment: Any significant similarity of a predicted protein sequence to a portion of

Query Match 9.9%; Score 8; DB 4; Length 627;
 Best Local Similarity 100.0%; Pred. No. 2.3; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 SLGDRRL 26
 Db 293 SLGDRRL 300

RESULT 4

QY 2 antigen - mouse (fragment)
 SL2268
 Qa 2 antigen - mouse (house mouse)
 C;Species: Mus musculus (house mouse)
 C;Accession: SL2268
 C;Species: Mus musculus (house mouse)
 C;Accession: SL2268
 R;Ulker, N.; Lewis, K.D.; Hood, L.E.; Stroynowski, I.
 EMBO J. 9, 3839-3847, 1990
 A;Title: Activated T cells transcribe an alternatively spliced mRNA encoding a solubl
 A;Reference number: SL2268; MUID:91005311; PMID:2246652
 A;Accession: SL2268
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-19 <ULK>
 A;Cross-references: GB:X57330; NID:9288506; PIDN:CAA40607.1; PID:9288508

Query Match 8.6%; Score 7; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 62 RWGGCGG 68
 Db 6 RWGGCGG 12

RESULT 5

B96038
 probable plasmid stability protein [imported] - Sinorhizobium meliloti (strain 1021):
 C;Species: Sinorhizobium meliloti
 C;Accession: B96038
 C;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing e
 A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: B96038
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-137 <KUR>
 A;Cross-references: GB:AL51985; PIDN:CAC49970.1; PID:915141458; GSPDB:GN00167
 A;Experimental source: strain 1021, megaplasmid pSymB
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Anpe, F.; Barloy-Hub
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9839-9844, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
 hebault, P.; Vandebol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 Science 293, 668-672, 2001

Best Local Similarity 100.0%; Pred. No. 15; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, M.; Stert, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193

A;Accession: AB2738

A;Status: preliminary

A;Residues: 1-214 <KUR>

A;Cross-references: GB:AE008688; PIDN:AA142320.1; PID:917739723; GSPDB:GN00186

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu114

A;Map position: circular chromosome

Query Match 8.6%; Score 7; DB 2; Length 214; Best Local Similarity 100.0%; Pred. No. 11; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 DTGGMFL 80
|||||||
Db 88 DTGGMFL 94

RESULT 11

14207 Invulin - dog

C;Species: Canis lupus familiaris (dog)

C;Accession: I46207

R;Tseng, H.; Green, H. Mol. Biol. Evol. 7, 293-302, 1990

A;Title: The invulin genes of pig and dog: comparison of their segments of repeats with the cornified cell envelope; duplication; epidermis; tandem repeat

A;Reference number: I46207; MUID:90348475; PMID:2385171

A;Accession: I46207

A;Status: translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-285 <TSE>

A;Cross-references: GB:NM3442; PIDN:9163980; PIDN:AAA30853.1; PID:9163981

C;Comment: During the terminal differentiation of keratinocytes, this protein from the linked envelope underlie the plasma membrane.

C;Superfamily: invulin

C;Keywords: cornified cell envelope; duplication; epidermis; tandem repeat

Query Match 8.6%; Score 7; DB 1; Length 285; Best Local Similarity 100.0%; Pred. No. 14; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 KQ00EQ 38
111111
Db 198 KQ00EQ 204

RESULT 12

H64156 hypothetical protein H0697 - Haemophilus influenzae (strain Rd K420)

C;Species: Haemophilus influenzae

C;Accession: I46156

R;Kleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Bruban, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: H64156

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-304 <TRGR>

A;Cross-references: GB:U32751; GB:L42023; PIDN:93212200; PIDN:AC23347.1; PID:91573689; T

A;Note: best homolog was a hypothetical protein from *Bacillus subtilis*

Query Match 8.6%; Score 7; DB 2; Length 304; Best Local Similarity 100.0%; Pred. No. 16; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 15; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFIVLIFI 13
|||||||
Db 71 LFIVLIFI 77

RESULT 13

C71612 multiple-TM membrane protein PFB0535w - malaria parasite (Plasmodium falciparum)

C;Species: Plasmodium falciparum

C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000

C;Accession: C71612

R;Gardiner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Perete, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H. Science 282, 1126-1132, 1998

A;Reference number: A71600; MUID:99021743; PMID:9804551

A;Accession: C71612

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-311 <GAR>

A;Cross-references: GB:AE001401; GB:AB001362; NID:93845209; PIDN: AAC71896.1; PID:9384

A;Experimental source: clone 3D7

A;Gene: PFB0535w

A;Genetics:

Query Match 8.6%; Score 7; DB 2; Length 311; Best Local Similarity 100.0%; Pred. No. 15; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFIVLIFI 13
|||||||
Db 205 LFIVLIFI 211

RESULT 14

S38166 hypothetical protein YKR088c - yeast (Saccharomyces cerevisiae)

C;Species: Saccharomyces cerevisiae

C;Accession: S38166

R;Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantale submitted to the Protein Sequence Database, March 1994

A;Reference number: S38158

A;Accession: S38166

A;Molecule type: DNA

A;Residues: 1-337 <BAL>

A;Cross-references: EMBL:228313; NID:9486572; PIDN:CAA82167.1; PID:9486573; MIPS:YKR088c

A;Experimental source: strain S288C

R;Garcia-Cantalejo, J.; Baladron, V.; Esteban, P.F.; Santos, M.A.; Bou, G.; Remacha, Yeast 10, 231-245, 1994

A;Title: The complete sequence of an 18,002 bp segment of *Saccharomyces cerevisiae* chromosome 14

A;Reference number: S42009; MUID:94262327; PMID:8203164

A;Accession: S42017

A;Molecule type: DNA

A;Residues: 1-337 <GAR>

A;Cross-references: EMBL:Z27116; NID:9415899; PIDN:CAA81639.1; PID:9415908

A;Experimental source: strain S288C

C;Genetics:

A;Cross-references: SGD:S0001796

A;Map position: I1R

C;Keywords: transmembrane protein

F_96-112/Domain: transmembrane #status predicted <TM1> F_138-154/Domain: transmembrane #status predicted <TM2> F_174-190/Domain: transmembrane #status predicted <TM3> F_290-306/Domain: transmembrane #status predicted <TM4>

Query Match 8.6%; Score 7; DB 2; Length 337; Best Local Similarity 100.0%; Pred. No. 16; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFIYLFI 13
||| |||
Db 264 LFIYLFI 270

RESULT 15

A54430 hypoxic function transcription repressor ROX1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: DNA-binding protein ROX1; protein YP9499.20; protein YPR065W
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: A54430; S54086; S55246; S17015
R;Balasubramanian, B.; Lowry, C.V.; Zitomer, R.S.
Mol. Cell. Biol. 13, 6071-6078, 1993
A;Title: The Rox1 repressor of the *Saccharomyces cerevisiae* hypoxic genes is a specific
A;Reference number: A54430; MOID:94019282; PMID:8413209
A;Accession: A54430
A;Molecule type: DNA
A;Residues: 1-368 <BAD>
A;Cross-references: EMBL:X60458; NID:94361; PIDN:CAA2991.1; PID:94362
R;Baddock, K.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54067
A;Accession: S54086
A;Molecule type: DNA
A;Residues: 1-368 <BAD>
A;Cross-references: EMBL:Z49219; NID:9805025; PIDN:CAA89182.1; PID:9805045; MIPS:YPR065W
R;Deeckert, J.; Perini, R.; Balasubramanian, B.; Zitomer, R.S.
Genetics 139, 1149-1158, 1995
A;Title: Multiple elements and auto-repression regulate Rox1, a repressor of hypoxic genes
A;Reference number: S55246; MOID:95286046; PMID:7768429
A;Accession: S55246
A;Molecule type: DNA
A;Residues: 1-17 <DEC>
C;Genetics:
A;Gene: SGD:ROX1
A;Cross-references: SGD:S0006269; MIPS:YPR065W
A;Map position: 16R
C;Superfamily: unassigned HMG box proteins; HMG box homology
C;Keywords: DNA binding; transcription regulation
F;8-87/Domain: HMG box homology <HMG1>

Query Match 8 6%; Score 7; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 QQQKEQQ 39
||| |||
Db 106 QQQKEQQ 112

Search completed: May 29, 2003, 15:33:24
Job time : 43 secs

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